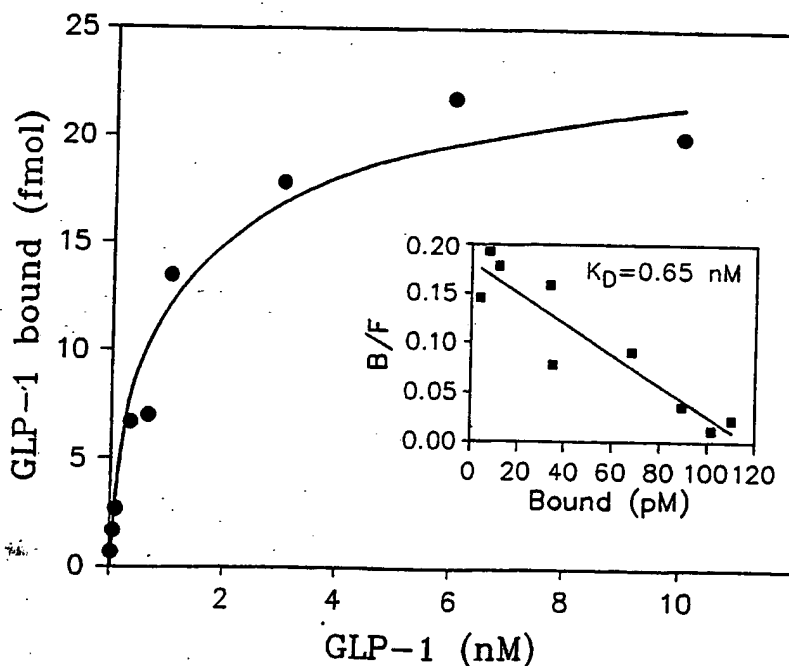


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**(54) Title:** RECEPTOR FOR THE GLUCAGON-LIKE-PEPTIDE-1 (GLP-1)**(57) Abstract**

The present invention relates to a recombinant glucagon-like peptide-1 (GLP-1) receptor, to a DNA construct which comprises a DNA sequence encoding a GLP-1 receptor, to methods of screening for agonists of GLP-1 activity, and to the use of the GLP-1 receptor for screening for agonists of GLP-1 activity.

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## RECEPTOR FOR THE GLUCAGON-LIKE-PEPTIDE-1 (GLP-1)

## FIELD OF THE INVENTION

The present invention relates to a recombinant glucagon-like peptide-1 (GLP-1) receptor, to a DNA construct which comprises a DNA sequence encoding a GLP-1 receptor, to methods of screening for agonists of GLP-1 activity, and to the use of the GLP-1 receptor for screening for agonists of GLP-1 activity.

## BACKGROUND OF THE INVENTION

As used in the present specification the designation GLP-1 comprises GLP-1(7-37) as well as GLP-1(7-36)amide.

Glucose-induced insulin secretion is modulated by a number of hormones and neurotransmitters. In particular, two gut hormones, glucagon-like peptide-1 (GLP-1) and gastric inhibitory peptide (GIP) potentiate the effect of glucose on insulin secretion and are thus called gluco-incretins (Dupre, in *The Endocrine Pancreas*, E. Samois Ed. (Raven Press, New York, (1991), 253 - 281) and Ebert and Creutzfeld, (*Diabetes Metab. Rev.* 3, (1987)). Glucagon-like peptide-1 is a gluco-incretin both in rat and in man (Dupre and Ebert and Creutzfeld, vide supra, and Kreymann et al. (*Lancet* 2 (1987), 1300)). It is part of the preproglucagon molecule (Bell et al. *Nature* 304 (1983), 368) which is proteolytically processed in intestinal L cells to GLP-1(1-37) and GLP-1(7-36)amide or GLP-1(7-37) (Mojsov et al. (*J.Biol.Chem.* 261 (1986), 11880) and Habener et al.: *The Endocrine Pancreas* E. Samois Ed. (Raven Press, New York (1991), 53 - 71). Only the truncated forms of GLP-1 are biologically active and both have identical effects on insulin secretion in beta cells (Mojsov et al. *J.Clin.Invest* 79 (1987), 616) and Weir et al. (*Diabetes* 38 (1989), 338). They are the most potent gluco-incretins so far described and are

active at concentrations as low as one to ten picomolar. The stimulatory effect of these gluco-incretin hormones requires the presence of glucose at or above the normal physiological concentration of about 5 mM and is mediated by activation of adenylate cyclase and a rise in the intracellular concentration of cyclic AMP (Drucker et al. Proc.Natl.Acad.Sci. USA 84 (1987), 3434) and Göke et al. (Am.J.Physiol. 257 (1989), G397). GLP-1 has also a stimulatory effect on insulin gene transcription (Drucker et al. Proc.Natl.Acad.Sci. USA 84 (1987), 3434). In a rat model of non-insulin-dependent diabetes mellitus (NIDDM) is associated with a reduced stimulatory effect of GLP-1 on glucose-induced insulin secretion (Suzuki et al. Diabetes 39 (1990), 1320). In man, in one study, GLP-1 levels were elevated in NIDDM patients both in the basal state and after glucose ingestion; however, following a glucose load there was only a very small rise in plasma insulin concentration (Ørskov et al. J.Clin.Invest. 87 (1991), 415). A recent study (Nathan et al. Diabetes Care 15 (1992), 270) showed that GLP-1 infusion could ameliorate postprandial insulin secretion and glucose disposal in NIDDM patients. Thus, as a further step in understanding the complex modulation of insulin secretion by gut hormones and its dysfunction in diabetes, we isolated and characterized a complementary DNA for the beta cell GLP-1 receptor and showed that it is part of a new family of G-coupled receptors.

#### DESCRIPTION OF THE INVENTION

The present invention relates to a recombinant glucagon-like peptide-1 (GLP-1) receptor.

More preferably, the invention relates to a GLP-1 receptor which comprises the amino acid sequence shown in SEQ ID No. 1, or an analogue thereof binding GLP-1 with an affinity constant,  $K_D$ , below 100 nM, preferably below 10 nM. In the present

context, the term "analogue" is intended to indicate a naturally occurring variant (including one expressed in other animal species, in particular human) of the receptor or a "derivative" i.e. a polypeptide which is derived from the native GLP-1 receptor by suitably modifying the DNA sequence coding for the variant, resulting in the addition of one or more amino acids at either or both the C- and N-terminal ends of the native amino acid sequence, substitution of one or more amino acids at one or more sites in the native amino acid sequence, deletion of one or more amino acids at either or both ends of the native sequence or at one or more sites within the native sequence, or insertion of one or more amino acids in the native sequence.

In another aspect, the present invention relates to a DNA construct which comprises a DNA sequence encoding the GLP-1 receptor of the invention, as well as a recombinant expression vector carrying the DNA construct and a cell containing said recombinant expression vector.

In one embodiment of the invention, the GLP-1 receptor molecule may be provided in solubilised and/or reconstituted form.

In the present context "solubilised" is intended to indicate a receptor as present in detergent-solubilised membrane preparations. "Reconstituted" is intended to indicate a receptor solubilised in the presence of essential cofactors, e.g. G-protein. In this embodiment the receptor may be in a reconstituted micellar form.

The DNA construct of the invention encoding the GLP-1 receptor preferably comprises the DNA sequence shown in SEQ ID No. 1, or at least a DNA sequence coding for a functional analogue thereof binding GLP-1 with an affinity below 100 nM, preferably below 10 nM or a suitable modification thereof. Examples of suitable modifications of the DNA sequence are nucleotide

substitutions which do not give rise to another amino acid sequence of the GLP-1 receptor, but which may correspond to the codon usage of the host organism into which the DNA construct is introduced or nucleotide substitutions which do give rise to a different amino acid sequence and therefore, possibly, a different protein structure without, however, impairing the properties of the native variant. Other examples of possible modifications are insertion of one or several nucleotides into the sequence, addition of one or several nucleotides at either end of the sequence, or deletion of one or several nucleotides at either end or within the sequence.

Another example of a DNA construct of the invention is one which encodes a GLP-1 receptor variant particularly suitable for solubilisation and reconstitution.

The DNA construct of the invention encoding the present GLP-1 receptor may be prepared synthetically by established standard methods, e.g. the phosphoramidite method described by Beaucage and Caruthers, Tetrahedron Letters 22 (1981), 1859 - 1869, or the method described by Matthes et al., EMBO Journal 3 (1984), 801 - 805. According to the phosphoramidite method, oligonucleotides are synthesized, e.g. in an automatic DNA synthesizer, purified, annealed, ligated and cloned in suitable vectors.

The DNA construct of the invention may also be of genomic or cDNA origin, for instance obtained by preparing a genomic or cDNA library and screening for DNA sequences coding for all or part of the GLP-1 receptor of the invention by hybridization using synthetic oligonucleotide probes in accordance with standard techniques (cf. Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor, 1989). In this case, a genomic or cDNA sequence encoding the GLP-1 receptor may be modified at a site corresponding to the site(s) at which it is desired to introduce amino acid substitutions, e.g. by

site-directed mutagenesis using synthetic oligonucleotides encoding the desired amino acid sequence for homologous recombination in accordance with well-known procedures.

Finally, the DNA construct may be of mixed synthetic and genomic, mixed synthetic and cDNA or mixed genomic and cDNA origin prepared by ligating fragments of synthetic, genomic or cDNA origin (as appropriate), the fragments corresponding to various parts of the entire DNA construct, in accordance with standard techniques. The DNA construct may also be prepared by polymerase chain reaction using specific primers, for instance as described in US 4,683,202 or Saiki et al., Science 239 (1988), 487 - 491.

The recombinant expression vector into which the DNA construct of the invention is inserted may be any vector which may conveniently be subjected to recombinant DNA procedures, and the choice of vector will often depend on the host cell into which it is to be introduced. Thus, the vector may be an autonomously replicating vector, i.e. a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g. a plasmid. Alternatively, the vector may be one which, when introduced into a host cell, is integrated into the host cell genome and replicated together with the chromosome(s) into which it has been integrated.

In the vector, the DNA sequence encoding the GLP-1 receptor of the invention should be operably connected to a suitable promoter sequence. The promoter may be any DNA sequence which shows transcriptional activity in the host cell of choice and may be derived from genes encoding proteins either homologous or heterologous to the host cell. Examples of suitable promoters for directing the transcription of the DNA encoding the GLP-1 receptor of the invention in mammalian cells are the SV40 promoter (Subramani et al., Mol. Cell Biol. 1 (1981), 854 -

864), the MT-1 (metallothionein gene) promoter (Palmiter et al., Science 222 (1983), 809 - 814) or the adenovirus 2 major late promoter. A suitable promoter for use in insect cells is the polyhedrin promoter (Vasuvedan et al., FEBS Lett. 311, 5 (1992) 7 - 11). Suitable promoters for use in yeast host cells include promoters from yeast glycolytic genes (Hitzeman et al., J. Biol. Chem. 255 (1980), 12073 - 12080; Alber and Kawasaki, J. Mol. Appl. Gen. 1 (1982), 419 - 434) or alcohol dehydrogenase genes (Young et al., in Genetic Engineering of 10 Microorganisms for Chemicals (Hollaender et al, eds.), Plenum Press, New York, 1982), or the TPI1 (US 4,599,311) or ADH2-4c (Russell et al., Nature 304 (1983), 652 - 654) promoters. Suitable promoters for use in filamentous fungus host cells are, for instance, the ADH3 promoter (McKnight et al., The EMBO 15 J. 4 (1985), 2093 - 2099) or the tpiA promoter.

The DNA sequence encoding the GLP-1 receptor of the invention may also be operably connected to a suitable terminator, such as the human growth hormone terminator (Palmiter et al., op. cit.) or (for fungal hosts) the TPI1 (Alber and Kawasaki, op. cit.) or ADH3 (McKnight et al., op. cit.) terminators. The vector may further comprise elements such as polyadenylation signals (e.g. from SV40 or the adenovirus 5 Elb region), transcriptional enhancer sequences (e.g. the SV40 enhancer) and translational enhancer sequences (e.g. the ones encoding 25 adenovirus VA RNAs).

The recombinant expression vector of the invention may further comprise a DNA sequence enabling the vector to replicate in the host cell in question. An example of such a sequence (when the host cell is a mammalian cell) is the SV40 origin of 30 replication. The vector may also comprise a selectable marker, e.g. a gene the product of which complements a defect in the host cell, such as the gene coding for dihydrofolate reductase (DHFR) or one which confers resistance to a drug, e.g. neomycin, hygromycin or methotrexate.



The procedures used to ligate the DNA sequences coding for the GLP-1 receptor of the invention, the promoter and the terminator, respectively, and to insert them into suitable vectors containing the information necessary for replication, are well known to persons skilled in the art (cf., for instance, Sambrook et al., op.cit.).

The host cell into which the expression vector of the invention is introduced may be any cell which is capable of producing the GLP-1 receptor of the invention and is preferably a eukaryotic cell, such as invertebrate (insect) cells or vertebrate cells, e.g. Xenopus laevis oocytes or mammalian cells, in particular insect and mammalian cells. Examples of suitable mammalian cell lines are the COS (ATCC CRL 1650), BHK (ATCC CRL 1632, ATCC CCL 10), CHL (ATCC CCL39) or CHO (ATCC CCL 61) cell lines. Methods of transfecting mammalian cells and expressing DNA sequences introduced in the cells are described in e.g. Kaufman and Sharp, J. Mol. Biol. 159 (1982), 601 - 621; Southern and Berg, J. Mol. Appl. Genet. 1 (1982), 327 - 341; Loyter et al., Proc. Natl. Acad. Sci. USA 79 (1982), 422 - 426; Wigler et al., Cell 14 (1978), 725; Corsaro and Pearson, Somatic Cell Genetics 7 (1981), 603, Graham and van der Eb, Virology 52 (1973), 456; and Neumann et al., EMBO J. 1 (1982), 841 - 845.

Alternatively, fungal cells (including yeast cells) may be used as host cells of the invention. Examples of suitable yeasts cells include cells of Saccharomyces spp. or Schizosaccharomyces spp., in particular strains of Saccharomyces cerevisiae. Examples of other fungal cells are cells of filamentous fungi, e.g. Aspergillus spp. or Neurospora spp., in particular strains of Aspergillus oryzae or Aspergillus niger. The use of Aspergillus spp. for the expression of proteins is described in, e.g., EP 272 277.

The GLP-1 receptor according to the invention may be produced by a method which comprises culturing a cell as described above

in a suitable nutrient medium under conditions which are conducive to the expression of the GLP-1 receptor, and recovering the GLP-1 receptor from the culture. The medium used to culture the cells may be any conventional medium suitable for growing mammalian cells, such as a serum-containing or serum-free medium containing appropriate supplements. Suitable media are available from commercial suppliers or may be prepared according to published recipes (e.g. in catalogues of the American Type Culture Collection).

- 10 If the GLP-1 receptor has retained the transmembrane and (possibly) the cytoplasmic region of the native variant, it will be anchored in the membrane of the host cell, and the cells carrying the GLP-1 receptor may be used as such in the screening or diagnostic assay. Alternatively, the receptor may  
15 be a component of membrane preparations, e.g. in solubilised and/or reconstituted form as defined above.

In a still further aspect, the present invention relates to a method of screening for agonists or enhancers of GLP-1 activity, the method comprising incubating a GLP-1 receptor  
20 according to any of claims 1 - 3 with a substance suspected to be an agonist of GLP-1 activity and subsequently with a GLP-1 or an analogue thereof, and detecting any effect from the suspected agonist on the binding of GLP-1 to the GLP-1 receptor. An enhancer being defined as a compound capable of  
25 stabilizing interaction between a high-affinity form of the receptor and the corresponding ligand, as described e.g. for the adenosin receptor (Bruns et al. Molecular Pharmacology 38 (1990), 939).

An alternative method of screening for agonists of GLP-1  
30 activity, comprises incubating GLP-1 or an analogue thereof with a substance suspected to be an agonist of GLP-1 activity and subsequently with a GLP-1 receptor of the invention, and detecting any effect on the binding to the GLP-1 receptor. Such

agonists of GLP-1 activity will be substances stimulating glucose-induced insulin secretion and may be used in the treatment of NIDDM.

The GLP-1 receptor may be immobilized on a solid support and may, as such, be used as a reagent in the screening methods of the invention. The GLP-1 receptor may be used in membrane-bound form, i.e. bound to whole cells or as a component of membrane preparations immobilised on a solid support.

The solid support employed in the screening methods of the invention preferably comprises a polymer. The support may in itself be composed of the polymer or may be composed of a matrix coated with the polymer. The matrix may be of any suitable material such as glass, paper or plastic. The polymer may be selected from the group consisting of a plastic (e.g. latex, a polystyrene, polyvinylchloride, polyurethane, polyacrylamide, polyvinylalcohol, nylon, polyvinylacetate, and any suitable copolymer thereof), cellulose (e.g. various types of paper, such as nitrocellulose paper and the like), a silicon polymer (e.g. siloxane), a polysaccharide (e.g. agarose or dextran), an ion exchange resin (e.g. conventional anion or cation exchange resins), a polypeptide such as polylysine, or a ceramic material such as glass (e.g. controlled pore glass).

The physical shape of the solid support is not critical, although some shapes may be more convenient than others for the present purpose. Thus, the solid support may be in the shape of a plate, e.g. a thin layer or microtiter plate, or a film, strip, membrane (e.g. a nylon membrane or a cellulose filter) or solid particles (e.g. latex beads or dextran or agarose beads). In a preferred embodiment, the solid support is in the form of wheat germ agglutinin-coated SPA beads (cf. US 4,568,649).

Alternatively, screening for GLP-1 agonists can also be carried out using a cell line expressing the cloned GLP-1 receptor functionally coupled to a G-protein. In living cells, exposure to an agonist will give rise to an increase in the  
5 intracellular cAMP concentration. The cAMP concentration can then be measured directly. Changes in cAMP levels may also be monitored indirectly using appropriate cell lines in which a measurable signal is generated in response to an increase in intracellular cAMP.

10 It is furthermore contemplated to locate the ligand-binding site on the GLP-1 receptor of the invention, for instance by preparing deletion or substitution derivatives of the native GLP-1 receptor (as described above) and incubating these with ligands known to bind the full-length GLP-1 receptor and  
15 detecting any binding of the ligand to the GLP-1 receptor deletion derivative. Once the ligand-binding site has been located, this may be used to acquire further information about the three-dimensional structure of the ligand-binding site. Such three-dimensional structures may, for instance, be  
20 established by means of protein engineering, computer modelling, NMR technology and/or crystallographic techniques. Based on the three-dimensional structure of the ligand-binding site, it may be possible to design substances which are agonists to the GLP-1 molecule.

25 The characterization of the GLP-1 receptor is of considerable physiological and pathological importance. It will help study a fundamental aspect of the entero-insular axis (Unger and Eisentraut, Arch.Int.Med. 123 (1969), 261): the potentiating effect of gut hormones on glucose-induced insulin secretion,  
30 the role of these hormones in the control of glucose homeostasis and also the possible therapeutic use of GLP-1 to stimulate insulin secretion in NIDDM patients (Mathan et al. Diabetes Care 15 (1992), 270). Investigation of the regulated expression and desensitization of the receptor in the normal

state and during the development of diabetes will contribute to a better understanding of the modulation of insulin secretion in normal and pathological situations. Availability of antibodies against this receptor may also allow an analysis of the surface localization of this receptor and its distribution relative to the beta cell glucose transporter GLUT2 (Thorens et al. Cell 55 (1988), 281 and Orci et al. Science 245 (1989), 295). This aspect pertains to the hypothesis that the beta cell membrane has a "regulatory" domain which contains hormone receptors (Bonner-Weir Diabetes 37 (1988), 616), and which may be distinct from GLUT2-containing membrane domains previously identified (Thorens et al. Cell 55 (1988), 281 and Orci et al. Science 245 (1989), 295). Finally, the identification of an additional member of this new family of G-coupled receptors will help design experiments to probe the structure-function relationship of these new molecules.

#### BRIEF DESCRIPTION OF THE DRAWINGS

The present invention is further illustrated in the following examples with reference to the appended drawings in which

Fig. 1A and Fig. 1B which is a continuation of Fig. 1A together show the amino acid sequence of the rat GLP-1 receptor in a comparison with the sequence of the rat secretin receptor (SECR), the opossum parathyroid hormone receptor (PTHr) and the porcine calcitonin receptor (CTR1). The GLP-1 receptor has three N glycosylation sites in the extracellular domain (arrows). Four cysteines are conserved at identical places in the four receptor (boxes). Note the otherwise very divergent sequences in this part of the molecules as well as in the COOH-terminal cytoplasmic tail. Sequence identities are denoted by stars and homologies by dots. The location of the putative transmembrane domains are indicated by horizontal bars above the sequences.

Fig. 2 shows binding of  $^{125}\text{I}$ -GLP-1 to COS cells transfected with the pGLPR-16 plasmid. Specific binding reaches saturation at 1 to 10 nM GLP-1. Insert: Scatchard analysis of GLP-1 binding.

5 Fig. 3 shows binding of  $^{125}\text{I}$ -GLP-1 to INS-1 cells. Specific binding reaches saturation at 1 to 10 nM GLP-1. Insert: Scatchard analysis of GLP-1 binding.

Fitting of the curves in Figs. 2 and 3 were performed with the LIGAND program (McPherson, Kinetic, EBDA, Ligand, Lowry. A  
10 Collection of radioligand analysis programs (Elsevier, Amsterdam, 1985)).

Fig. 4 shows displacement of  $^{125}\text{I}$ -GLP-1 binding to COS cells transfected with the rat GLP-1 receptor cDNA. Transfected cells were incubated with 20 pM  $^{125}\text{I}$ -GLP-1 in the presence of  
15 increasing concentrations of cold peptides. Each point was measured in duplicate and the experiments repeated three times for GLP-1, GIP and glucagon and once for VIP and secretin.

Fig. 5 shows stimulation of cyclic AMP formation in COS cells transfected with the rat GLP-1 receptor cDNA. COS cells were  
20 transfected with the pcDNA-1 vector alone (open bars) or the pGLPR-1 plasmid (stripped bar) and incubated in the absence or the presence of GLP-1 at the indicated concentration. cAMP production was measured in triplicate with a radioimmunoassay (Amersham).

25 Fig. 6 shows tissue specificity of GLP-1 receptor expression assessed by Northern blotting of RNA from different tissues and from the INS-1 cell line. Ten micrograms of total RNA was analyzed on each lane. Two major RNA species of 2.7 and 3.6 kb were detected in all tissues in which the receptor was  
30 detected. The position of the migration of the ribosomal RNAs is indicated to the left of the picture.

Fig. 7 is a comparison of the rat GLP-1 receptor amino acid sequence (rat) and a partial amino acid sequence of the human GLP-1 receptor (human).

The present invention is further illustrated in the following examples which is not intended to be in any way limiting to the scope of the invention as claimed.

#### EXAMPLE 1

##### Molecular Cloning and Characterisation of the Rat Islet GLP-1 Receptor cDNA.

10 A rat pancreatic islet cDNA library was constructed in the pcDNA-1 expression vector (Rat pancreatic islets were prepared according to Gotoh et al. (Transplantation 43 (1985), 725). PolyA+ RNA was prepared and the cDNA library was constructed in the pcDNA-1 vector (In Vitrogen) as described by Aruffo and  
15 Seed (Proc.Natl.Acad.Sci. USA 84 (1987), 8573) and Lin et al. (Proc.Natl.Acad.Sci. USA 88 (1991), 3185). Plasmid DNA was prepared from pools of five to eight thousands bacterial clones (Maniatis et al., Molecular Cloning. A Laboratory Manual. Cold Spring Harbor Laboratory, 1982) and transfected into COS cells  
20 (Sompayrac and Dana, Proc.Natl.Acad.Sci. USA 78 (1981), 7575). The presence of GLP-1 receptor expressed in COS cells was assessed by binding of the radioiodinated peptide followed by photographic emulsion autoradiography and screening by dark field microscopy (Gearing et al. EMBO J. 8 (1989), 3667). GLP-  
25 1(7-36)amide, as well as the other peptides, were purchased from Peninsula Laboratories. Iodination was performed by the iodine monochloride method (Contreras et al. Meth.Enzymol. 92 (1983), 277), the peptide was purified by passage over Sephadex G-10 followed by CM-Sepharose and specific activity was  
30 determined by the self displacement technique (Calvo et al. Biochem. 212 (1983), 259). A 1.6 kb cDNA clone (pGLPR-1) was isolated by subfractionation of an original positive pool and

was used to isolate, by DNA hybridization screening, two additional clones from primary positive pools. These plasmids (pGLPR-16 and -87) had inserts of 3.0 and 2.0 kb, respectively. Transfection of these clones into COS cells generated high affinity ( $K_D = 0.6$  nM) binding sites for GLP-1 (Fig. 2). This affinity is comparable to that seen for binding of GLP-1 to the rat insulinoma cell line INS-1 (Asfari et al. *Endocrinology* 130 (1992), 167) ( $K_D = 0.12$  nM; Fig. 3). In both cases a single high affinity binding component was detected. The binding to GLP-1 receptor transfected COS cells reached a plateau between 1 and 10 nM. At concentrations above 10 nM a second, high capacity, low affinity, binding component was detected. Although specifically displacable by cold GLP-1, this binding was also present in COS cells transfected with the expression vector alone and was therefore not further characterized.

Binding of GLP-1 to the receptor expressed in COS cells was displaced by cold GLP-1 with a 50 percent displacement achieved at 0.5 to 1 nM (Fig. 4). Other peptide hormones of related structure such as secretin, gastric inhibitory peptide (GIP) and vasoactive intestinal peptide (VIP) (Dupre in *The Endocrine Pancreas*, E. Samois Ed. (Raven Press, New York, (1991), 253 - 281) and Ebert and Creutzfeld, *Diabetes Metab. Rev.* 3, (1987) did not displace binding. Glucagon could displace the binding by 50 percent but only at a concentration of one micromolar (Fig. 4). The addition of subnanomolar concentrations of GLP-1 to transfected COS cells stimulated the production of cyclic AMP indicating that the receptor was functionally coupled to activation of adenylate cyclase (Fig. 5).

DNA sequence analysis of the rat GLP-1 receptor cDNA revealed a major open reading frame coding for a 463 amino acid polypeptide (SEQ ID No. 1). Hydrophaphy plot analysis indicated the presence of an amino-terminal hydrophobic region most probably representing a leader sequence. This hydrophobic segment is followed by a hydrophilic domain of about 120 amino



acids which contains three N-linked glycosylation sites. Seven hydrophobic segments are present which may form transmembrane domains. Search for sequence identities showed the GLP-1 receptor to be homologous to the secretin receptor (Ishihara et al. EMBO J. 10 (1991), 1635) (40 percent identity), the parathyroid hormone receptor (Jüppner et al. (Science 254 (1991), 1024) (32.4 percent identity) and the calcitonin receptor (Lin et al. Science 254 (1991), 1022) (27.5 percent identity) (Fig. 1). These four receptors do not share any significant sequence homology with other known members of the G-coupled receptor family and are characterized by a relatively long amino terminal, probably extracellular, domain. The sequence of the extracellular domain is unique for each receptor, yet four cysteines are perfectly conserved (boxes in Fig. 1). A fifth cysteine at position 126 of the GLP-1 receptor is also conserved in the parathyroid and calcitonin receptors and at a similar location in the secretin receptor (position 123). The highest sequence identity between the four proteins resides in the transmembrane domains. The carboxyl terminal, cytoplasmic, ends of each receptor are also very different. These receptors all stimulate the production of cyclic AMP in response to ligand binding (Ishihara et al. EMBO J. 10 (1991), 1635), Jüppner et al. (Science 254 (1991), 1024) and Lin et al. Science 254 (1991), 1022) and are presumably coupled to the cyclase via  $G_{\alpha}$ . In that respect, it is interesting to note that a sequence motif present in the third cytoplasmic loop of the GLP-1 receptors (RLAK, present just before the sixth transmembrane domain) is very similar to a motif of the beta2 adrenergic receptor (KALK) present at the same location and whose basic amino acids have been shown to be important in the coupling of the receptor to  $G_{\alpha}$  (Okamoto et al. Cell 67 (1991); 723). Moreover, in the beta2 adrenergic receptor, this motif is preceded by a basic amino acid located twelve amino acid toward the amino-terminal end. This basic amino acid is also required at this particular distance for efficient coupling to  $G_{\alpha}$ . In the GLP-1 receptor a lysine residue is also present at

a similar location. This suggests that, despite the very low overall sequence identity, a structural feature may have been conserved in the third cytoplasmic loop between the two receptors which, may be required for the coupling of receptor to the Gs $\alpha$  protein.

Determination of the tissue distribution of the GLP-1 receptor was performed by Northern blot analysis. Northern blot analysis was performed with 10  $\mu$ g of total RNA (Chomczynski and Sacchi, Anal.Biochem. 126 (1987), 156) denatured with glyoxal (McMaster and Carmichael, Proc.Natl.Acad.Sci. USA 74 (1977), 4835) separated on a 1% agarose gel and transferred to Nylon membranes (Thomas, Proc.Natl.Acad.Sci. USA 77 (1980), 5201). Hybridization was performed with the random primed labelled (Feinberg and Vogelstein, Anal.Biochem. 132 (1983), 6) 1,6 kb pGLPR-1 insert. Two mRNAs of 2.7 and 3.6 kb could be detected in pancreatic islets as well as in rat insulinoma cell lines (INS-1), in stomach and in lung (Fig. 6). No GLP-1 receptor mRNA could be detected in brain, liver, thymus, muscle, intestine and colon. The presence of the GLP-1 receptor has been reported in stomach where the peptide inhibits acid secretion by parietal cells in *in vivo* experiments (Schjoldager et al. Dig.Dis.Sci. 34 (1989), 703) but stimulates acid secretion on isolated parietal glands (Schmidtler et al. Am.J.Physiol. 260 (1991), G940). Binding sites for GLP-1 have also been reported in lung membrane preparations (Richter et al. FEBS Letter 1 (1990), 78) but the role of the hormone on lung physiology is not known.

A stable cell line expressing the cloned rat GLP-1 receptor was established by Ca-phosphate mediated transfection (Maniatis et al., Molecular Cloning. A Laboratory Manual. Cold Spring Harbour Laboratory, 1989) of the CHL cell line (ATCC CCL39). The plasmid, pGLPR-1, which contains a 1.6 kb rat GLP-1 receptor cDNA insert cloned in the pCDNA-1 vector, was cotransfected with the pWL-neo plasmid (Stratagene, La Jolla,

CA) into CHL cells. The pWL-neo plasmid contains the neomycin resistance gene. Stable clones were selected in medium containing 0.8 mg/ml G418. A stable transformant expressing an estimate of 70.000 rat GLP-1 receptors pr cell was selected by this scheme and further propagated in the presence of 80  $\mu$ M G418. Membranes from this transformant was subsequently used in the high-volume-throughput-screening (HVTS) assay as described in Example 3. Characterization of the receptor expressed by the GLP-1 R/CHL cell line led to an estimated Kd of 0.8 nM for whole cells, 2.3 nM for cell membranes using  $^{125}$ I-GLP-1(7-36)amide as radioligand.

#### EXAMPLE 2

##### Molecular cloning of the human islet GLP-1 receptor cDNA.

Human islets were prepared as described (Ricordi et al., Diabetes 37 (1988), 413 - 420), and poly-A<sup>+</sup> RNA was isolated by affinity chromatography by published methods (Gonda et al., Mol. Cell. Biol. 2 (1982) 617 - 624).

A human islet cDNA library was constructed in the  $\lambda$ ZAPII vector from Stratagene (La Jolla, CA). Briefly, double stranded cDNA was synthesized as previously described (Aruffo and Seed, 84 (1987), 8573 - 8577; Thorens, Proc. Natl. Acad. Sci., USA 89 (1992), 8641 - 8645), and EcoRI/NotI adaptors (Stratagene, La Jolla, CA) were added with T<sub>4</sub> DNA ligase.

The resulting cDNA molecules were phosphorylated with T<sub>4</sub> polynucleotide kinase before size fractionation on potassium acetate gradients (Aruffo and Seed, 84 (1987), 8573 - 8577). Double stranded cDNA with a size above 1.6 kb was ligated into  $\lambda$ ZAPII arms (Stratagene, La Jolla, CA), packaged in  $\lambda$  phage and grown on a lawn of XL-1 Blue E. coli cells as described in protocols from Stratagene.

The cDNA library was screened by hybridization to a  $^{32}$ P labelled

DNA fragment from the rat GLP-1 receptor cDNA by previously described methods (Maniatis et al., Molecular Cloning. A Laboratory Manual. Cold Spring Harbour Laboratory, 1982).

The reduced stringency conditions used were: prehybridization and hybridization in 30 % formamide, 5 \* SSC, 5 \* Denhardt, 50 mM phosphate buffer pH 6.8, 5 mM EDTA, 0.2 % SDS and 100 µg/ml salmon sperm DNA at 42°C. Washings were 4 \* 30 min in 2 \* SSC, 0.2 % SDS at 42°C (Maniatis et al., Molecular Cloning. A Laboratory Manual. Cold Spring Harbour Laboratory, 1982).

10 Positive λ phages were purified by replating and hybridization, the cDNA inserts contained in the Bluescript vector present in the λ ZAPII arms were excised using helper phages obtained from Stratagene (La Jolla, CA). The inserts were partially sequenced. One clone designated 3(20) showed high homology to  
15 the rat GLP-1 receptor and was sequenced (Tabor and Richardson, Proc. Natl. Acad. Sci., USA 84 (1987), 4767 - 4771) in its entire length. The DNA sequence is shown as SEQ ID No. 3.

From homology analysis (Fig. 7), it was concluded that this cDNA encoded the 3' part of the human GLP-1 receptor.

20 The deduced amino acid sequence of the human receptor has 92 % identity to the rat GLP-1 receptor in the region from amino acid number 170 to amino acid number 463 (numbers refer to the rat sequence).

The isolated human GLP-1 cDNA does not contain the entire open  
25 reading frame at the 5' end. However, a full length clone can easily be obtained by methods well known to persons skilled in the art. Among the alternative methods of choice, the following examples should be mentioned: 1) The human islet cDNA library can either be rescreened with a probe from the 5' end of the  
30 already cloned sequence. 2) Anchor-PCR or RACE (Rapid Amplification of cDNA Ends) (Kriangkum et al., Nucleic Acids Res. 20 (1992) 3793 - 3794; Troutt et al., Proc. Natl. Acad. Sci., USA 89 (1992), 9823 - 9825) methodology can be used to

clone the remaining 5' sequences from islet RNA. 3) The remaining 5' part can be isolated from human genomic libraries, and DNA fragments considered to represent introns can be identified based on homology to the cDNA of the rat receptor and deleted by mutagenesis.

After cloning of the 5' end of the open reading frame, this part of the cDNA can be fused to the remaining 3' part of the human GLP-1 receptor cDNA by the use of PCR or through fusion at appropriate restriction enzyme recognition sequences identified in both the 5' and the 3' parts.

The cDNA encoding the full length open reading frame can be cloned in suitable mammalian expression vectors and transfected into mammalian cell lines for expression. Examples of such suitable cell lines are the CHO and CHL cells, but other mammalian cells will also express receptors of this type.

It has recently been demonstrated that insect cells (Vasudevan et al. FEBS Lett. 311 (1992), 7 - 11) and microorganisms like e.g. yeast (King et al., Science 250 (1990), 121 - 123) can express G-protein coupled receptors.

Recently frog skin melanophore cells have been used to express G-protein coupled receptors (Potenza et al, Analytical Biochem., 206, (1992), 315 - 322) and a functional coupling to adenylate cyclase was demonstrated.

Other microorganisms like Aspergillus, Bacillus, E. coli might be able to express these receptors after appropriate genetic engineering and selection.

It is therefore clear to persons skilled in the art that a number of different expression systems can be designed that will lead to expression of a functional receptor molecule.

As demonstrated in Example 3, the rat as well as the human GLP-1 receptor can be used in screening assays for detection of new potential agonist lead structures.

### EXAMPLE 3

#### 5 High throughput screening assay for GLP-1 receptor agonists.

Screening of microbial extracts for secondary metabolites with potential GLP-1 agonist activity was carried out using the SPA (Scintillation Proximity Assay) technology (US patent 4568649, Hart and Greenwalt (Mol.Immunol., 16 (1979) 265-267), Udenfri-  
10 end et al (Proc.Natl.Acad.Sci. USA, 82 (1985) 8672-8676). Wheatgerm agglutinin (WGA) coated SPA beads developed by Amersham International were used (US. patent 4568649, European patent 0154734, Japanese patent appl. 84/52452). The WGA coat allows GLP-1 receptor bearing membranes to be immobilized on  
15 the SPA beads. Membranes used in the screening assay were prepared from a CHL (ATTC CCL39) cell line expressing the cloned rat GLP-1 receptor as described in in Example 1. Membranes were prepared essentially as described by Uden et al (Eur.J.Biochem. 145 (1984), 525-530). The binding of <sup>125</sup>I-GLP-  
20 1(7-36)amide to such immobilized receptors brings the tracer in close proximity to the scintillant present within the SPA beads resulting in the emission of light. Any unbound ligand will not generate a signal. Thus under assay conditions a microbial extract - containing a component capable of binding to the GLP-  
25 1 receptor and thereby displacing the tracer - may be identified by virtue of a reduction in signal intensity.

A high throughput assay was established using 96 well microtiter plates. The assay was optimized with regard to the amounts of WGA particles, membrane and tracer used. (The <sup>125</sup>I-  
30 GLP-1(7-36)amide tracer was labelled using the lactoperoxidase method (Morrison et al., Methods Enzymol. 70 (1980), 214-219) followed by purification on reverse phase HPLC). Using a Pac-

kard TopCount™ microplate scintillation counter (Packard Instrument Company) these optimized conditions resulted in a  $B_0$  of more than 7000 cpm. (Non specific binding determined in the presence of 500 nM unlabelled GLP-1(7-36)amide amounts to less than 1000 cpm.  $IC_{50}=0.5-1.0$  nM GLP-1(7-36) amide).

So far 1250 microbial extracts have been screened using the SPA GLP-1 receptor assay. The extracts were tested at a final dilution of 1:400. Under these conditions 15 out of the 1250 extracts resulted in a reduction of specific counts to below the chosen cut-off level. These 15 hits have been further characterized in a secondary assay. This secondary assay was designed to test whether cAMP synthesis in a GLP-1 receptor bearing cell line can be induced by components in the extract.  $\beta$ -TC3 cells (Hanahan et al., Nature 315 (1985) 115-122) and Efrat et al (Proc.Natl.Acad.Sci. USA 85 (1988) 9037-9041) grown in 96-well microtiter plates were exposed to extracts diluted in culture media. After 20 min at 37°C the cells were lysed by addition of acid and the cAMP concentration determined using the cyclic AMP SPA system (Amersham International). Of the 15 primary hits tested in this secondary assay, 5 extracts have been found to significantly increase the cAMP level in  $\beta$ -TC3 cells.

It has thus been demonstrated that it is feasible that the screening approach described in this patent application can result in the isolation of natural compounds with GLP-1 agonist activity. The use of such compounds as lead structures for a medicinal chemistry approach will be of significant importance in the design of novel GLP-1 agonists.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Thorens, Bernard

(ii) TITLE OF INVENTION: Novel Peptide

5 (iii) NUMBER OF SEQUENCES: 4

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: NOVO NORDISK A/S, Patent Department

(B) STREET: Novo Alle

10 (C) CITY: Bagsvaerd

(E) COUNTRY: Denmark

(F) ZIP: DK-2880

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

15 (B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

20 (B) FILING DATE:

(C) CLASSIFICATION:

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: +45 44 44 88 88

(B) TELEFAX: +45 44 49 32 56

25 (C) TELEX: 37307

## (2) INFORMATION FOR SEQ ID NO:1:



23

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3066 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

5 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Rat

## 10 (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 17..1408

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCCTGAGCGC CCCGCC ATG GCC GTC ACC CCC AGC CTG CTG CGC CTG GCG	49
15 Met Ala Val Thr Pro Ser Leu Leu Arg Leu Ala	
1 5 10	
CTC CTG CTG CTC GGG GCG GTG GGC AGG GCC GGC CCC CGC CCC CAG GGT	97
Leu Leu Leu Leu Gly Ala Val Gly Arg Ala Gly Pro Arg Pro Gln Gly	
15 20 25	
20 GCC ACG GTG TCC CTC TCA GAG ACA GTG CAG AAA TGG AGA GAG TAT CGG	145
Ala Thr Val Ser Leu Ser Glu Thr Val Gln Lys Trp Arg Glu Tyr Arg	
30 35 40	
CAC CAG TGC CAA CGT TTC CTC ACG GAA GCG CCA CTC CTG GCC ACA GGT	193
His Gln Cys Gln Arg Phe Leu Thr Glu Ala Pro Leu Leu Ala Thr Gly	
25 45 50 55	

24

	CTC	TTC	TGC	AAC	CGA	ACC	TTT	GAT	GAC	TAC	GCC	TGC	TGG	CCA	GAT	GGG	241
	Leu	Phe	Cys	Asn	Arg	Thr	Phe	Asp	Asp	Tyr	Ala	Cys	Trp	Pro	Asp	Gly	
	60					65					70					75	
	CCC	CCA	GGT	TCC	TTT	GTG	AAT	GTC	AGT	TGC	CCC	TGG	TAC	CTG	CCG	TGG	289
5	Pro	Pro	Gly	Ser	Phe	Val	Asn	Val	Ser	Cys	Pro	Trp	Tyr	Leu	Pro	Trp	
					80					85						90	
	GCC	AGT	AGT	GTG	CTC	CAA	GGG	CAT	GTG	TAC	CGG	TTC	TGC	ACG	GCC	GAG	337
	Ala	Ser	Ser	Val	Leu	Gln	Gly	His	Val	Tyr	Arg	Phe	Cys	Thr	Ala	Glu	
					95				100						105		
10	GGT	ATC	TGG	CTG	CAT	AAG	GAC	AAC	TCC	AGC	CTG	CCC	TGG	AGG	GAC	CTG	385
	Gly	Ile	Trp	Leu	His	Lys	Asp	Asn	Ser	Ser	Leu	Pro	Trp	Arg	Asp	Leu	
		110						115						120			
	TCG	GAG	TGC	GAA	GAG	TCC	AAG	CAA	GGA	GAG	AGA	AAC	TCC	CCT	GAG	GAA	433
	Ser	Glu	Cys	Glu	Glu	Ser	Lys	Gln	Gly	Glu	Arg	Asn	Ser	Pro	Glu	Glu	
15		125					130					135					
	CAG	CTC	CTG	TCG	CTG	TAC	ATT	ATC	TAC	ACG	GTG	GGG	TAC	GCA	CTT	TCT	481
	Gln	Leu	Leu	Ser	Leu	Tyr	Ile	Ile	Tyr	Thr	Val	Gly	Tyr	Ala	Leu	Ser	
	140					145					150					155	
	TTC	TCT	GCC	TTG	GTC	ATC	GCT	TCA	GCC	ATC	CTT	GTC	AGC	TTC	AGA	CAC	529
20	Phe	Ser	Ala	Leu	Val	Ile	Ala	Ser	Ala	Ile	Leu	Val	Ser	Phe	Arg	His	
					160					165					170		
	TTG	CAC	TGC	ACC	AGG	AAC	TAC	ATC	CAC	CTG	AAC	CTG	TTT	GCG	TCC	TTC	577
	Leu	His	Cys	Thr	Arg	Asn	Tyr	Ile	His	Leu	Asn	Leu	Phe	Ala	Ser	Phe	
					175				180					185			
25	ATC	CTC	CGA	GCA	CTG	TCC	GTC	TTC	ATC	AAA	GAC	GCT	GCC	CTC	AAG	TGG	625
	Ile	Leu	Arg	Ala	Leu	Ser	Val	Phe	Ile	Lys	Asp	Ala	Ala	Leu	Lys	Trp	
		190						195						200			

25

	ATG TAT AGC ACG GCT GCG CAA CAG CAC CAG TGG GAT GGG CTC CTC TCG	673
	Met Tyr Ser Thr Ala Ala Gln Gln His Gln Trp Asp Gly Leu Leu Ser	
	205 210 215	
	TAT CAG GAC TCT CTG GGC TGC CGA CTG GTG TTC CTG CTC ATG CAA TAC	721
5	Tyr Gln Asp Ser Leu Gly Cys Arg Leu Val Phe Leu Leu Met Gln Tyr	
	220 225 230 235	
	TGC GTG GCG GCC AAC TAC TAC TGG TTG CTG GTG GAA GGC GTG TAT CTG	769
	Cys Val Ala Ala Asn Tyr Tyr Trp Leu Leu Val Glu Gly Val Tyr Leu	
	240 245 250	
10	TAC ACA CTG CTG GCC TTC TCG GTG TTC TCG GAG CAG CGC ATC TTC AAG	817
	Tyr Thr Leu Leu Ala Phe Ser Val Phe Ser Glu Gln Arg Ile Phe Lys	
	255 260 265	
	CTG TAC CTG AGC ATA GGC TGG GGA GTT CCG CTG CTG TTC GTT ATC CCC	865
	Leu Tyr Leu Ser Ile Gly Trp Gly Val Pro Leu Leu Phe Val Ile Pro	
15	270 275 280	
	TGG GGC ATT GTC AAG TAT CTC TAC GAG GAC GAG GGT TGC TGG ACC AGG	913
	Trp Gly Ile Val Lys Tyr Leu Tyr Glu Asp Glu Gly Cys Trp Thr Arg	
	285 290 295	
	AAC TCC AAC ATG AAC TAT TGG CTC ATC ATA CGC TTG CCC ATT CTC TTT	961
20	Asn Ser Asn Met Asn Tyr Trp Leu Ile Ile Arg Leu Pro Ile Leu Phe	
	300 305 310 315	
	GCA ATC GGG GTC AAC TTC CTT GTC TTC ATC CGG GTC ATC TGC ATC GTG	1009
	Ala Ile Gly Val Asn Phe Leu Val Phe Ile Arg Val Ile Cys Ile Val	
	320 325 330	

26

	ATA GCC AAG CTG AAG GCT AAT CTC ATG TGT AAG ACC GAC ATC AAA TGC	1057
	Ile Ala Lys Leu Lys Ala Asn Leu Met Cys Lys Thr Asp Ile Lys Cys	
	335 340 345	
	AGA CTC GCG AAG TCC ACT CTG ACG CTC ATC CCG CTT CTG GGC ACG CAT	1105
5	Arg Leu Ala Lys Ser Thr Leu Thr Leu Ile Pro Leu Leu Gly Thr His	
	350 355 360	
	GAA GTC ATC TTT GCC TTT GTG ATG GAC GAG CAC GCC CGA GGA ACC CTA	1153
	Glu Val Ile Phe Ala Phe Val Met Asp Glu His Ala Arg Gly Thr Leu	
	365 370 375	
10	CGC TTC GTC AAG CTG TTC ACA GAG CTC TCC TTC ACT TCC TTC CAG GGC	1201
	Arg Phe Val Lys Leu Phe Thr Glu Leu Ser Phe Thr Ser Phe Gln Gly	
	380 385 390 395	
	TTT ATG GTG GCT GTC TTG TAC TGC TTT GTC AAC AAT GAG GTC CAG ATG	1249
	Phe Met Val Ala Val Leu Tyr Cys Phe Val Asn Asn Glu Val Gln Met	
15	400 405 410	
	GAG TTT CGG AAG AGC TGG GAG CGC TGG AGG CTG GAG CGC TTG AAC ATC	1297
	Glu Phe Arg Lys Ser Trp Glu Arg Trp Arg Leu Glu Arg Leu Asn Ile	
	415 420 425	
	CAG AGG GAC AGC AGC ATG AAA CCC CTC AAG TGT CCC ACC AGC AGC GTC	1345
20	Gln Arg Asp Ser Ser Met Lys Pro Leu Lys Cys Pro Thr Ser Ser Val	
	430 435 440	
	AGC AGT GGG GCC ACG GTG GGC AGC AGC GTG TAT GCA GCC ACC TGC CAA	1393
	Ser Ser Gly Ala Thr Val Gly Ser Ser Val Tyr Ala Ala Thr Cys Gln	
	445 450 455	
25	AAT TCC TGC AGC TGAGCCCCAG TGCTGCGCTT CCTGATGGTC CTTGCTGCTG	1445
	Asn Ser Cys Ser	
	460	

GCTGGGTGGC CATCCCAGGT GGGAGAGACC CTGGGGACAG GGAATATGAG GGATACAGGC 1505

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CCTCCTGGGA CCACAGACAC ATGTTCTCCA AGGAGAACAG CCTGCTAATT TAATCTCAGG 1685

5 CGACAGGAAG AGAGGAAGAA ACAATTGCTG TTAAGACGAG GAGGACTTCT TCCTGTAAAA 1745

GCTGCAAGGC CCTTGGGGTT CCCTCGGACA GAACTGCAAA TCAACCCCGG AACTCTCGCT 1805

CAAGGGCAAT TGCTGACGGG TGGAAGTTGG GCTTGCGAGA GGAGGCAGGT CCATGAGAGA 1865

CCTGCCCTTG GAACCTCAGC CAGCACAGCG CTCATCAAGG TGAGCTGGCT GTGCTGTGTG 1925

CACGGCTGGG GTTGTACCT ACATCAGCCT TCCTCTCGGA CAAGAGGCTT TTCTCTGTGC 1985

10 ATCTGGAGTG CCGCCATTCC TCCATCTGCC CGTTCATCCG CCATCCTGTC TTTGCCCTGG 2045

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GCCTGGTCCT TTAAGCCACT TTGCTGCTTG GTTTCTGCCC TGCATGGGTA CTAAGAGGC 2225

AGGTCCCAAG TTGAGAAGCC CAGAGGTGAG GTGTGAACCC TCAGTTCTGT TGTAAGATG 2285

15 CTCAAATACC CTCTAAGGT CATCTAAAGG AGTAACCTGC CTAGGGGTGC TGTTGACCTG 2345

AAATCAAGAG GACCAAAGGA TCCATTGCCA ACACCCCCCA TCCCCACAC ACACCTCATC 2405

TGTGACCAGA GTCTATGCTT TGAATCAGAA TGGGCTATAT CCTCTGACCT CAGAGGCTAT 2465

GACCCAGAAG AGATTCTTCC CTGAATCCTC CCACTTTGCA CACATATAGA CTTTATCCTT 2525

28

CTTCACTCTG TGTCTATTCA AACGTATAAT TCTGGTTTCT CTCACCCAC GGAAGAACTA 2585  
GATCACAGCA ACTGTTATGT TTGAGGGAGT GGGGGAGAAG GTGATTGATT TGACCCCTC 2645  
TCCCCACCG GTGTTGATAA GTAGCGTCTG TCCCACCTCC AGACTCCACC CACACATAAT 2705  
GAGCAGCACA TAGACCAGGA TGGGGGGGGT GGTATATCAT GCTTGCCCTC CTCCAACCAC 2765  
5 TATGAGAAGG CTAGCAGAAG ACACCACTGC ACAGACCCAA GTCCAAGGAC TGCCTCCCAG 2825  
GGAATTAGGC AGTGA CTTC TAGAGGCCAA GAAAGACTCC AAGAGCTGGA GAAGAATCCT 2885  
AGTCGATCTG GATCTCTTTT GAGGTTGGGG TTGGGGTGGC TTTCAATGGA TTCTCTCATG 2945  
AGGCTTATCT CTCCTCATC CCGTGGAGAG TGGGGGACCC TCCCTAGTGC TCACACTAGA 3005  
CACTGTGCCC CTTGGAGAGG CATAAGGCAT GTATGGGAGA TAATAATGGG CTATAAAACA 3065  
10 T 3066

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 463 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Val Thr Pro Ser Leu Leu Arg Leu Ala Leu Leu Leu Gly  
1 5 10 15

29

Ala Val Gly Arg Ala Gly Pro Arg Pro Gln Gly Ala Thr Val Ser Leu  
 20 25 30

Ser Glu Thr Val Gln Lys Trp Arg Glu Tyr Arg His Gln Cys Gln Arg  
 35 40 45

5 Phe Leu Thr Glu Ala Pro Leu Leu Ala Thr Gly Leu Phe Cys Asn Arg  
 50 55 60

Thr Phe Asp Asp Tyr Ala Cys Trp Pro Asp Gly Pro Pro Gly Ser Phe  
 65 70 75 80

Val Asn Val Ser Cys Pro Trp Tyr Leu Pro Trp Ala Ser Ser Val Leu  
 10 85 90 95

Gln Gly His Val Tyr Arg Phe Cys Thr Ala Glu Gly Ile Trp Leu His  
 100 105 110

Lys Asp Asn Ser Ser Leu Pro Trp Arg Asp Leu Ser Glu Cys Glu Glu  
 115 120 125

15 Ser Lys Gln Gly Glu Arg Asn Ser Pro Glu Glu Gln Leu Leu Ser Leu  
 130 135 140

Tyr Ile Ile Tyr Thr Val Gly Tyr Ala Leu Ser Phe Ser Ala Leu Val  
 145 150 155 160

Ile Ala Ser Ala Ile Leu Val Ser Phe Arg His Leu His Cys Thr Arg  
 20 165 170 175

Asn Tyr Ile His Leu Asn Leu Phe Ala Ser Phe Ile Leu Arg Ala Leu  
 180 185 190

Ser Val Phe Ile Lys Asp Ala Ala Leu Lys Trp Met Tyr Ser Thr Ala  
 195 200 205

30

Ala Gln Gln His Gln Trp Asp Gly Leu Leu Ser Tyr Gln Asp Ser Leu  
 210 215 220

Gly Cys Arg Leu Val Phe Leu Leu Met Gln Tyr Cys Val Ala Ala Asn  
 225 230 235 240

5 Tyr Tyr Trp Leu Leu Val Glu Gly Val Tyr Leu Tyr Thr Leu Leu Ala  
 245 250 255

Phe Ser Val Phe Ser Glu Gln Arg Ile Phe Lys Leu Tyr Leu Ser Ile  
 260 265 270

Gly Trp Gly Val Pro Leu Leu Phe Val Ile Pro Trp Gly Ile Val Lys  
 10 275 280 285

Tyr Leu Tyr Glu Asp Glu Gly Cys Trp Thr Arg Asn Ser Asn Met Asn  
 290 295 300

Tyr Trp Leu Ile Ile Arg Leu Pro Ile Leu Phe Ala Ile Gly Val Asn  
 305 310 315 320

15 Phe Leu Val Phe Ile Arg Val Ile Cys Ile Val Ile Ala Lys Leu Lys  
 325 330 335

Ala Asn Leu Met Cys Lys Thr Asp Ile Lys Cys Arg Leu Ala Lys Ser  
 340 345 350

Thr Leu Thr Leu Ile Pro Leu Leu Gly Thr His Glu Val Ile Phe Ala  
 20 355 360 365

Phe Val Met Asp Glu His Ala Arg Gly Thr Leu Arg Phe Val Lys Leu  
 370 375 380

Phe Thr Glu Leu Ser Phe Thr Ser Phe Gln Gly Phe Met Val Ala Val  
 385 390 395 400



31

Leu Tyr Cys Phe Val Asn Asn Glu Val Gln Met Glu Phe Arg Lys Ser  
405 410 415

Trp Glu Arg Trp Arg Leu Glu Arg Leu Asn Ile Gln Arg Asp Ser Ser  
420 425 430

5 Met Lys Pro Leu Lys Cys Pro Thr Ser Ser Val Ser Ser Gly Ala Thr  
435 440 445

Val Gly Ser Ser Val Tyr Ala Ala Thr Cys Gln Asn Ser Cys Ser  
450 455 460

(2) INFORMATION FOR SEQ ID NO:3:

- 10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1909 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- 15 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

- 20 (A) NAME/KEY: CDS  
(B) LOCATION: 3..887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

32

TC AGA CAC CTG TAC TGC ACC AGG AAC TAC ATC CAC CTG AAC CTG TTT Arg His Leu Tyr Cys Thr Arg Asn Tyr Ile His Leu Asn Leu Phe 1 5 10 15	47
GCA TCC TTC ATC CTG CGA GCA TTG TCC GTC TTC ATC AAG GAC GCA GCC 5 Ala Ser Phe Ile Leu Arg Ala Leu Ser Val Phe Ile Lys Asp Ala Ala 20 25 30	95
CTG AAG TGG ATG TAT AGC ACA GCC GCC CAG CAG CAC CAG TGG GAT GGG Leu Lys Trp Met Tyr Ser Thr Ala Ala Gln Gln His Gln Trp Asp Gly 35 40 45	143
10 CTC CTC TCC TAC CAG GAC TCT CTG AGC TGC CGC CTG GTG TTT CTG CTC Leu Leu Ser Tyr Gln Asp Ser Leu Ser Cys Arg Leu Val Phe Leu Leu 50 55 60	191
ATG CAG TAC TGT GTG GCG GCC AAT TAC TAC TGG CTC TTG GTG GAG GGC Met Gln Tyr Cys Val Ala Ala Asn Tyr Tyr Trp Leu Leu Val Glu Gly 15 65 70 75	239
GTG TAC CTG TAC ACA CTG CTG GCC TTC TCG GTG TTC TCT GAG CAA TGG Val Tyr Leu Tyr Thr Leu Leu Ala Phe Ser Val Phe Ser Glu Gln Trp 80 85 90 95	287
ATC TTC AGG CTC TAC GTG AGC ATA GGC TGG GGT GTT CCC CTG CTG TTT 20 Ile Phe Arg Leu Tyr Val Ser Ile Gly Trp Gly Val Pro Leu Leu Phe 100 105 110	335
GTT GTC CCC TGG GGC ATT GTC AAG ATC CTC TAT GAG GAC GAG GGC TGC Val Val Pro Trp Gly Ile Val Lys Ile Leu Tyr Glu Asp Glu Gly Cys 115 120 125	383
25 TGG ACC AGG AAC TCC AAC ATG AAC TAC TGG CTC ATT ATC CGG CTG CCC Trp Thr Arg Asn Ser Asn Met Asn Tyr Trp Leu Ile Ile Arg Leu Pro 130 135 140	431

	ATT CTC TTT GCC ATT GGG GTG AAC TTC CTC ATC TTT GTT CGG GTC ATC	479
	Ile Leu Phe Ala Ile Gly Val Asn Phe Leu Ile Phe Val Arg Val Ile	
	145 150 155	
	TGC ATC GTG GTA TCC AAA CTG AAG GCC AAT GTC ATG TGC AAG ACA GAC	527
5	Cys Ile Val Val Ser Lys Leu Lys Ala Asn Val Met Cys Lys Thr Asp	
	160 165 170 175	
	ATC AAA TGC AGA CTT GCC AAG TCC ACG CTG ACA CTC ATC CCC CTG CTG	575
	Ile Lys Cys Arg Leu Ala Lys Ser Thr Leu Thr Leu Ile Pro Leu Leu	
	180 185 190	
10	GGG ACT CAT GAG GTC ATC TTT GCC TTT GTG ATG GAC GAG CAC GCC CGG	623
	Gly Thr His Glu Val Ile Phe Ala Phe Val Met Asp Glu His Ala Arg	
	195 200 205	
	GGG ACC CTG CGC TTC ATC AAG CTG TTT ACA GAG CTC TCC TTC ACC TCC	671
	Gly Thr Leu Arg Phe Ile Lys Leu Phe Thr Glu Leu Ser Phe Thr Ser	
15	210 215 220	
	TTC CAG GGG CTG ATG GTG GCC ATC TTA TAC TGC TTT GTC AAC AAT GAG	719
	Phe Gln Gly Leu Met Val Ala Ile Leu Tyr Cys Phe Val Asn Asn Glu	
	225 230 235	
	GTC CAG CTG GAA TTT CGG AAG AGC TGG GAG CGC TGG CGG CTT GAG CAC	767
20	Val Gln Leu Glu Phe Arg Lys Ser Trp Glu Arg Trp Arg Leu Glu His	
	240 245 250 255	
	TTG CAC ATC CAG AGG GAC AGC AGC ATG AAG CCC CTC AAG TGT CCC ACC	815
	Leu His Ile Gln Arg Asp Ser Ser Met Lys Pro Leu Lys Cys Pro Thr	
	260 265 270	
25	AGC AGC CTG AGC AGT GGA GCC ACG GCG GGC AGC AGC ATG TAC ACA GCC	863
	Ser Ser Leu Ser Ser Gly Ala Thr Ala Gly Ser Ser Met Tyr Thr Ala	
	275 280 285	

ACT TGC CAG GCC TCC TGC AGC TGAGACTCCA GCGCCTGCCC TCCCTGGGGT 914  
Thr Cys Gln Ala Ser Cys Ser  
290 295

CCTTGCTGCG GCCGGGTGGC AATCCAGGAG AAGCAGCCTC CTAATTTGAT CACAGTGGCG 974

5 AGAGGAGAGG AAAAACGATC GCTGTGAAAA TGAGGAGGAT TGCTTCTTGT GAAACCACAG 1034

GCCCTTGGGG TTCCCCAGA CAGAGCCGCA AATCAACCCC AGACTCAAAC TCAAGGTCAA 1094

CGGCTTATTA GTGAAACTGG GGCTTGCAAG AGGAGGTGGT TCTGAAAGTG GCTCTTCTAA 1154

CCTCAGCCAA ACACGAGCGG GAGTGACGGG AGCCTCCTCT GCTTGCATCA CTTGGGGTCA 1214

CCACCCTCCC CTGTCTTCTC TCAAAGGGAA GCTGTTTGTG TGTCTGGGTT GCTTATTTCC 1274

10 CTCATCTTGC CCCCTCATCT CACTGCCCAG TTTCTTTTGG AGGGCTTGTT GGCCACTGCC 1334

AGCAGCTGTT TCTGGAAATG GCTGTAGGTG GTGTTGAGAA AGAATGAGCA TTGAGACACG 1394

GTGCTCGCTT CTCCTCCAGG TATTTGAGTT GTTTTGGTGC CTGCCTCTGC CATGCCCAGA 1454

GAATCAGGGC AGGCTTGCCA CCGGGGAACC CAGCCCTGGG GTATGAGCTG CCAAGTCTAT 1514

TTTAAAGACG CTCAAGAATC CTCTGGGGTT CATCTAGGGA CACGTTAGGA ATGTCCAGAC 1574

15 TGTGGGTGTA GGTTACCTGC CACTTCCAGG ACGCAGAGGG CCAAGAGAGA CATTGCCTCC 1634

ACCTCTCCTG AATACTTATC TGTGACCACA CGCTGTCTCT TGAGATTTGG ATACACTCTC 1694

TAGCTTTAGG GGACCATGAA GAGACTCTCT TAGGAAACCA ATAGTCCCCA TCAGCACCAT 1754

GGAGGCAGGC TCCCCCTGCC TTTGAAATTC CCCCATTGG GAGCTGATAT ACTTCACTCA 1814

CTTTTCTTTA TTGCTGTGAT AGTCTGTGTG CACAATGGGC AATTCTGACT TCTCCCATCT 1874

35

AGTGAAATGA GCGAAATCAT GGTGTAGTG ATCTT

1909

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 amino acids

5 (B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg	His	Leu	Tyr	Cys	Thr	Arg	Asn	Tyr	Ile	His	Leu	Asn	Leu	Phe	Ala	10	1		5		10		15
Ser	Phe	Ile	Leu	Arg	Ala	Leu	Ser	Val	Phe	Ile	Lys	Asp	Ala	Ala	Leu		20		25		30		
Lys	Trp	Met	Tyr	Ser	Thr	Ala	Ala	Gln	Gln	His	Gln	Trp	Asp	Gly	Leu		35		40		45		
Leu	Ser	Tyr	Gln	Asp	Ser	Leu	Ser	Cys	Arg	Leu	Val	Phe	Leu	Leu	Met	15	50		55		60		
Gln	Tyr	Cys	Val	Ala	Ala	Asn	Tyr	Tyr	Trp	Leu	Leu	Val	Glu	Gly	Val		65		70		75		80
Tyr	Leu	Tyr	Thr	Leu	Leu	Ala	Phe	Ser	Val	Phe	Ser	Glu	Gln	Trp	Ile	20		85		90		95	
Phe	Arg	Leu	Tyr	Val	Ser	Ile	Gly	Trp	Gly	Val	Pro	Leu	Leu	Phe	Val		100		105		110		

Val	Pro	Trp	Gly	Ile	Val	Lys	Ile	Leu	Tyr	Glu	Asp	Glu	Gly	Cys	Trp		
115					120					125							
Thr	Arg	Asn	Ser	Asn	Met	Asn	Tyr	Trp	Leu	Ile	Ile	Arg	Leu	Pro	Ile		
130					135					140							
s	Leu	Phe	Ala	Ile	Gly	Val	Asn	Phe	Leu	Ile	Phe	Val	Arg	Val	Ile	Cys	
145					150					155						160	
Ile	Val	Val	Ser	Lys	Leu	Lys	Ala	Asn	Val	Met	Cys	Lys	Thr	Asp	Ile		
165					170					175							
Lys	Cys	Arg	Leu	Ala	Lys	Ser	Thr	Leu	Thr	Leu	Ile	Pro	Leu	Leu	Gly		
10	180					185					190						
Thr	His	Glu	Val	Ile	Phe	Ala	Phe	Val	Met	Asp	Glu	His	Ala	Arg	Gly		
195					200					205							
Thr	Leu	Arg	Phe	Ile	Lys	Leu	Phe	Thr	Glu	Leu	Ser	Phe	Thr	Ser	Phe		
210					215					220							
15	Gln	Gly	Leu	Met	Val	Ala	Ile	Leu	Tyr	Cys	Phe	Val	Asn	Asn	Glu	Val	
225					230					235						240	
Gln	Leu	Glu	Phe	Arg	Lys	Ser	Trp	Glu	Arg	Trp	Arg	Leu	Glu	His	Leu		
245					250					255							
His	Ile	Gln	Arg	Asp	Ser	Ser	Met	Lys	Pro	Leu	Lys	Cys	Pro	Thr	Ser		
20	260					265					270						
Ser	Leu	Ser	Ser	Gly	Ala	Thr	Ala	Gly	Ser	Ser	Met	Tyr	Thr	Ala	Thr		
275					280					285							
Cys	Gln	Ala	Ser	Cys	Ser												
290																	

## CLAIMS

1. A recombinant glucagon-like peptide-1 (GLP-1) receptor.
2. A GLP-1 receptor according to claim 1 of mammalian origin.
- 5 3. A GLP-1 receptor according to claim 2 of rat or human origin.
4. A GLP-1 receptor according to claim 3, which comprises the amino acid sequence shown in SEQ ID No. 1, or an analogue thereof binding GLP-1 with an affinity constant below 100 nM,  
10 preferably below 10 nM.
5. A GLP-1 receptor according to claim 3, which comprises the partial amino acid sequence shown in SEQ ID No. 3, or an analogue thereof binding GLP-1 with an affinity constant below 100 nM, preferably below 10 nM.
- 15 6. A GLP-1 receptor according to any of the claims 1 to 5, which is in a solubilised or reconstituted form.
7. A DNA construct which comprises a DNA sequence encoding a GLP-1 receptor according to any of the claims 1 to 6.
8. A DNA construct according to claim 7, which comprises the  
20 DNA sequence shown in SEQ ID No. 1, or a DNA sequence coding for a functional analogue thereof binding GLP-1 with an affinity constant below 100 nM, preferably below 10 nM.
9. A DNA construct according to claim 7, which comprises the partial DNA sequence shown in SEQ ID No. 3, or a DNA sequence  
25 coding for a functional analogue thereof binding GLP-1 with an affinity constant below 100 nM, preferably below 10 nM.

10. A recombinant expression vector which carries an inserted DNA construct according to any of claims 7 to 9.
11. A cell containing a recombinant expression vector according to claim 10.
- 5 12. A cell containing a DNA construct according to any of claims 7 to 9 integrated in its genome.
13. A cell according to claim 11 or 12, which is an eukaryotic cell, in particular an insect or a mammalian cell.
14. A method of screening for agonists or enhancers of GLP-1  
10 activity, the method comprising incubating a GLP-1 receptor according to any of claims 1 to 6 with a substance suspected to be an agonist of GLP-1 activity and subsequently with a GLP-1 or an analogue thereof, and detecting any effect of binding of GLP-1 or the analogue to the GLP-1 receptor.
- 15 15. A method of screening for agonists or enhancers of GLP-1 activity, the method comprising incubating GLP-1 or an analogue thereof with a substance suspected to be an agonist of GLP-1 activity and subsequently with a GLP-1 receptor of the invention, and detecting any effect of binding of GLP-1 or the  
20 analogue to the receptor.
16. Use of a GLP-1 receptor according to any of claims 1 to 6 for screening for agonists of GLP-1 activity.
17. Use of DNA constructs according to claims 7 to 9 for isolation of tissue and/or organ specific variants of the GLP-1  
25 receptor.
18. Use of a receptor isolated according to claim 17 for the screening of GLP-1 agonists.



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GLPR	MAVTP-----SLLR-----LALLLLGAVGRAGPRPQGA-----	28
SECR	MLSTM RPR-LSLLL-----LRLLLLTKAAHTV-----GV-----	28
PTHR	MGAPRISHSLALLLCCSVLSSVYALVDADDVITKEEQIILLRNAQAQCEQEL	52
CTR1	MRFTLTRWCLTLFIFLNRPLPVLPSADGAHTPTLEPEPFLY-----	42
	* . . . . *	

GLPR	-----TVSLSETVQKWREYRHQCQRFLTE-----APLLATGLF	61
SECR	-----PPRLCDVRRVLLEERAHCLQQLSKEK-----KGALGPETASG--	65
PTHR	KEVLRVPELAESA KDWMSRS AKTKKEKPAEKLYPQAEESREVS DRSRLQDGF	104
CTR1	--ILGKQRM-----LEAQHRC-----Y-----DRMQKLPPYQGEGLY	72

GLPR	↓	C	NRTFDDYA	C	WPDGPPGSFVNVS	C	PWYLPWASSVLQGHVYRF	C	T	105
SECR		C	EGLWDNMS	C	WPSSAPARTVEVR	C	PKSLLSLSNK-NGSLFRN	C	T	108
PTHR		C	LPEWDNIV	C	WPAGVPGKVVAVP	C	PDYFYDFNHK--GRAYRR	C	D	146
CTR1		C	NRTWDGWS	C	WDDTPAGVLAEQY	C	PDYFPDFDA--AEKVTKY	C	G	114
		*	. * .	*	* . . . .	*	* . . . .	*	.	

GLPR	↓	AEGIWLHKDNSSLPWRDLSECEESKQGERNSPEEQLLSLYIIYTVGYALSFS	157
SECR		QDG-W----SETFPRPD LACGVNINNSFNERRHAYLLKLKVMYTVGYSSSLA	155
PTHR		SNGSWELVPGNNRTWANYSECVKFLTNETREREV-FDRLGMIYTVGYSLG	197
CTR1		EDGDWYRH PESNISWSNYTMCNAFTP--DKLQNAVYI--LYYLAIVGHSLSIL	162
		* * . . . . .	

		II	
GLPR	ALVIASAILVSFRHLHCTRNYIHLNLFASFILRALS VFIKDAALKWMYSTAA	209	
SECR	MLLVALSILCSFRRLHCTRNYIHMHLFVSFILRALS NF I KDAVL---FSSDD	204	
PTHR	SLTVAVLILGYFRRLHCTRNYIHMHLFVSFMLRAVSIFIKDAVLYSGVSTDE	249	
CTR1	TLLISLGIFMFLRSISCQRVTLHKNMFLTYVLNSIIIIVHLVVI-----	206	
	* . . * . . . . .		

		III	
GLPR	QQHQWDG-LLSY--QDS-----LGCRLVFLLMQYCVAANYWLLVEGVYLY	252	
SECR	-----VTYCDAHK-----VGCKLVMIFFQY C I M A N Y A W L L V E G L Y L H	241	
PTHR	I E R I T E E L R A F T E P P P A D K A G F V G C R V A T V F L Y F L T T N Y Y W I L V E G L Y L H	301	
CTR1	---VPNGELVK-RDPPI-----CKVLHFFHQYMMSCNYFWMLCEGVYLY	246	
		* . . * . . . . .	

Fig. 1A

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## IV

GLPR	TLLAFSVFSEQRIFKLYLSIGWGVPLLFVIPWGI <sup>2</sup> VKYLYEDEGCWTRNSNMN	304
SECR	TLLAISFFSERKYLQAFVLLGWGSPAIFVALWAI <sup>3</sup> TRHFL <sup>4</sup> ENTGCWDINANAS	293
PTHR	SLIFMAFFSEKKYLWGFTLFGWGLPAVFVAVVTV <sup>5</sup> VRATLANTECWDLSSGNK	353
CTR1	TLIVSVVFAEGQRLWWYHVLGWGFPLIPTTAHAIT <sup>6</sup> TRANLFNDNCW-LSVDTN	297
	. *. . *. . . . . *** * . . . . . **	

**V**

GLPR	YWLIIRLPILFAIGVNFVLFIRVICIVIAKLANLMCKTDIKC---RLAKST	353
SECR	VWWVIRGPVILSILINFIFFINILRILMRKLRTQETRGSETNH-YKRLAKST	344
PTHR	KW-IIQVPILAAIVVNFIILFINIIRVLATKLRETNAGRCDTROQYRKLLKST	404
CTR1	LLYIIHGVPVMAALVVNFFFLNILRVLVKKLKESQE---AESHMYLKAVRAT	346
	. *. * . . . * . . . * . . . * . . . *	

## VI

## VIT

[illegible]

GLPR	NNEVQMEFRKSWERWRL-RLNIQRDSSMKPLKC-----	438
SECR	NGEVQLEVQKKWRQWHLQ-EFPLRPVAFNNSFSN-----	424
PTHR	NGEVQAEIKKSWRWTALDFKRKARSGSSTYSYGPMSHTSVTNVGPGRGL	508
CTR1	NHEVQGALKRQWNQ-----YQAQRWAGRRS----TRAANAAAAATAAAAAAL	437
	* * * * *	

GLPR	-----PTSSVSSGATV-----	449
SECR	-----ATNGPTHSTKA-----	435
PTHR	ALSLSPRLAPGAGASANGHHQLPGYVKHGSISENSLPSSGPEPGTKDDGYLN	560
CTR1	AETV-----EIPVYICHQEPREP---AGEEPPVVEVEG---	467

GLPR	GSSVYAATC-----QNSCS	463
SECR	STEQSR SIP-----RASII	449
PTHR	GSGLYEP MVGEQPP LLEEERETVM	585
CTR1	-----VEVIAMEVLEOE--TSA	482

**Fig. 1B**

# SUBSTITUTE SHEET

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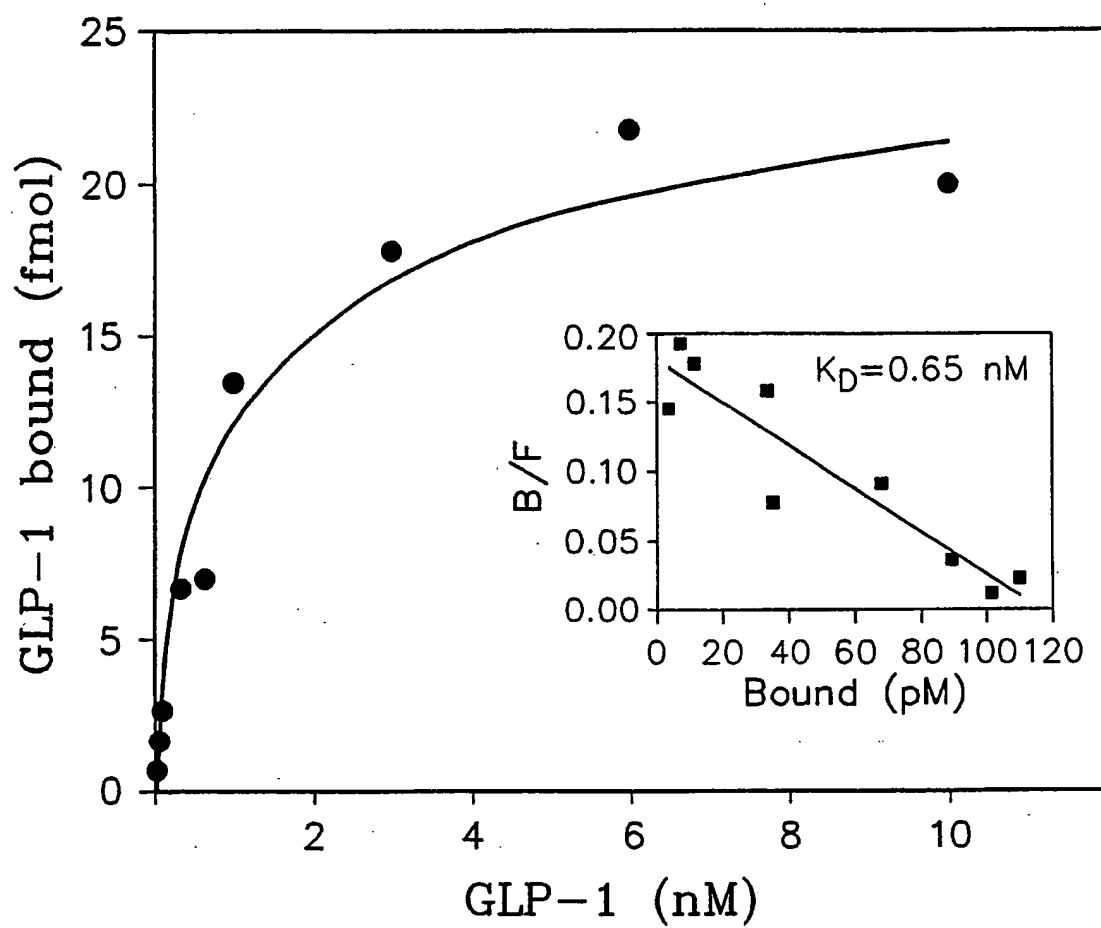


FIG. 2

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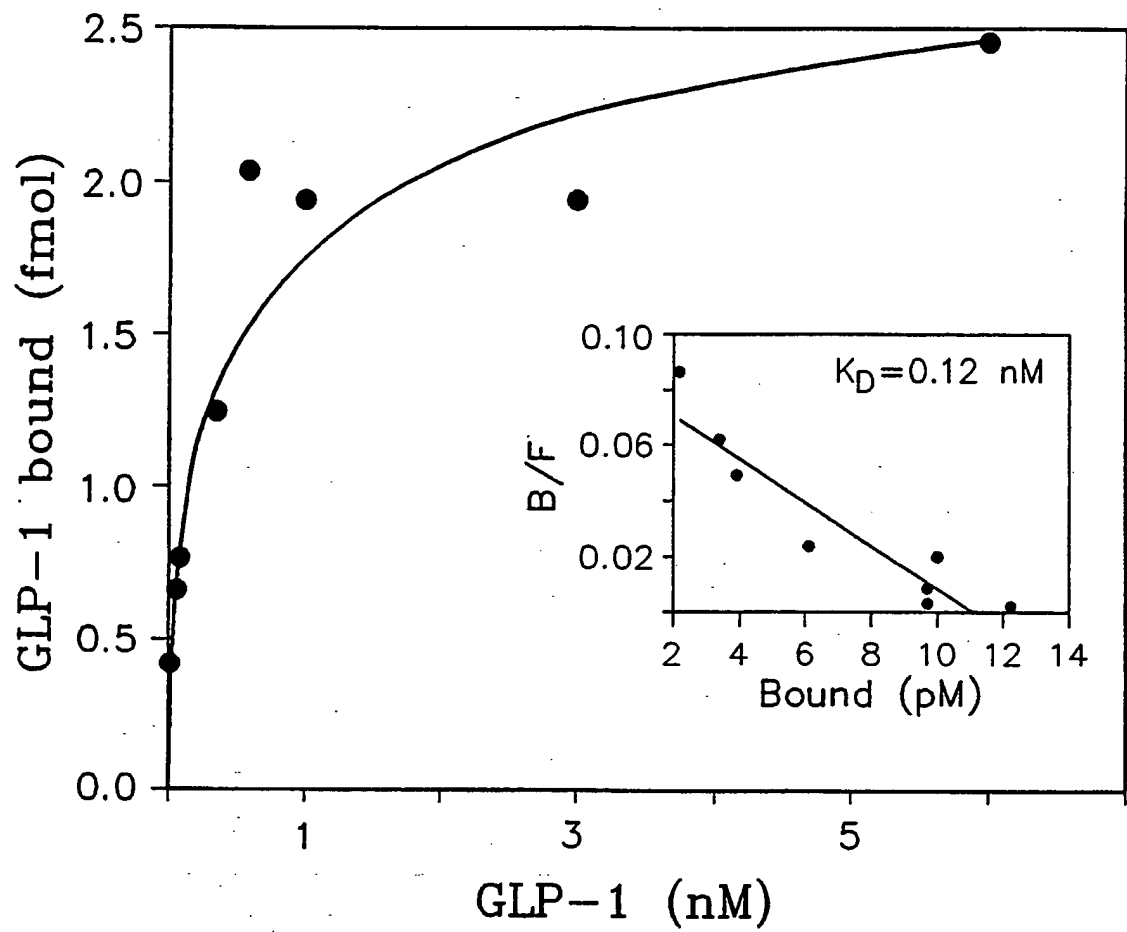


FIG. 3

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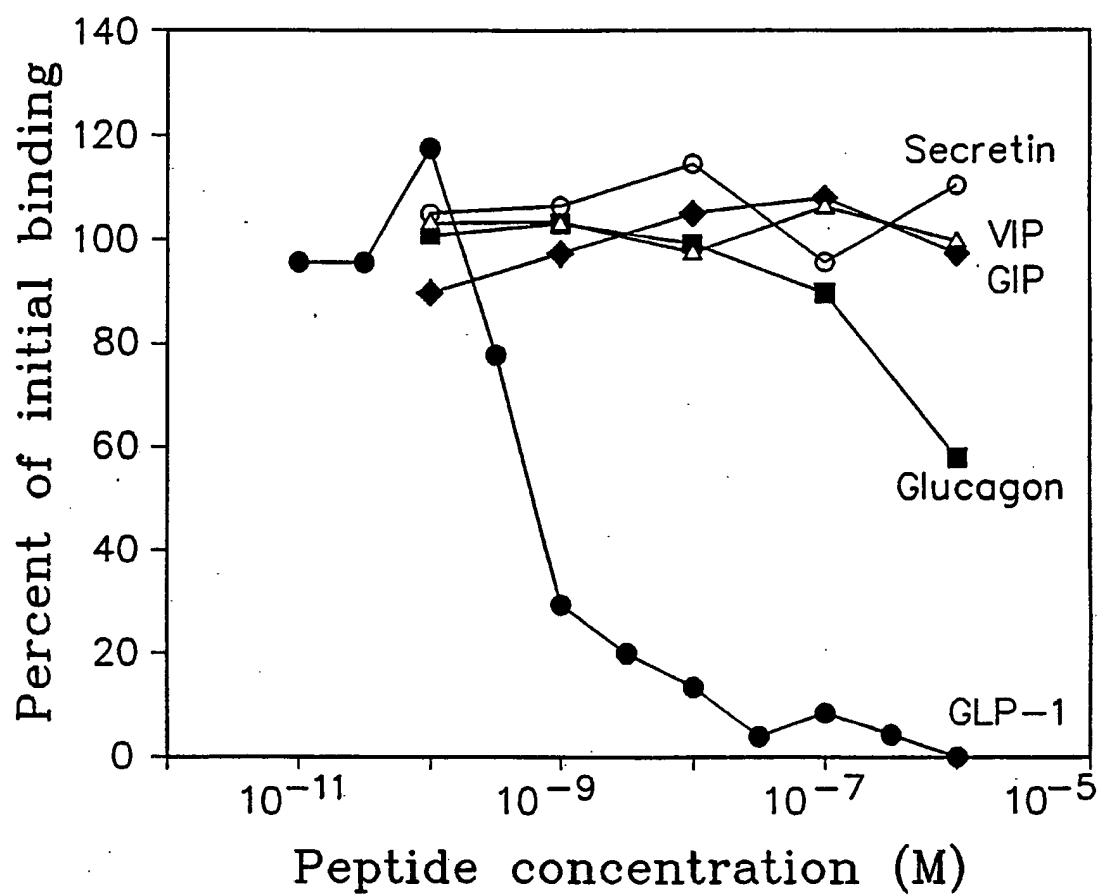


FIG. 4

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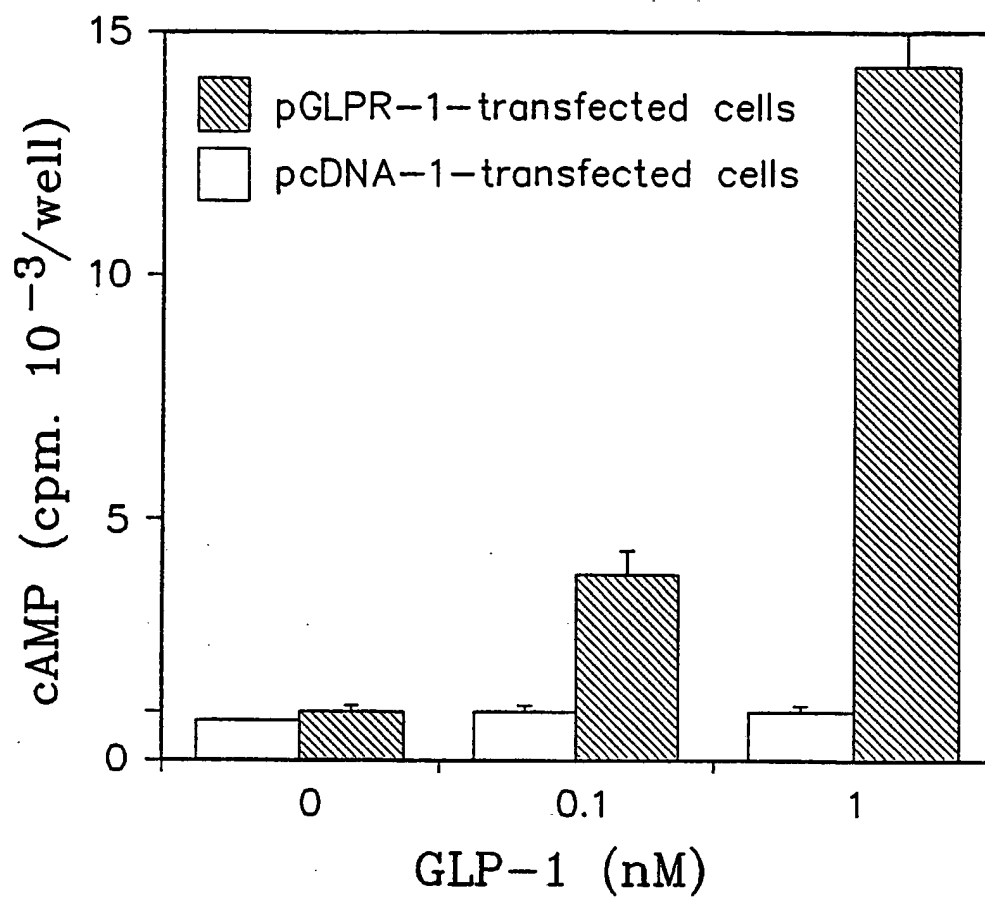


FIG. 5

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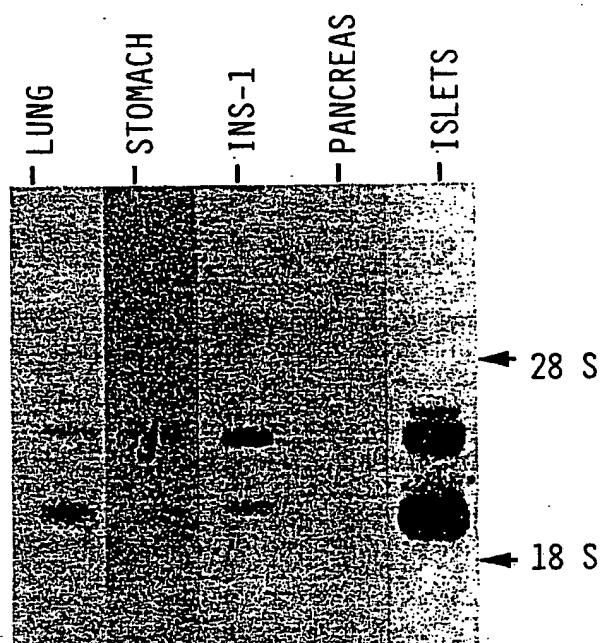


FIG. 6

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RAT - MAVTPSLLRLALLLLGAVGRAGPRPQGATVSLSETVQKWREYRHQCQRFL - 50  
 RAT - TEAPLLATGLFCNRTFDDYACWPDGPPGSFVNVSCPWYLPWASSVLQGHV -100  
 RAT - YRFCTAEGIWHLKDNSSLPWRDLSECEESKQGERNSPEEQLLSLYIIYTV -150  
 RAT - GYALSFSALVIASAILVSFRHLHCTRNYIHLNLFASFILRALSVFIKDAA -200  
 HUM - RHLYCTRNYIHLNLFASFILRALSVFIKDAA - 31  
 RAT - LKWMYSTAAQQHQWDGLLSYQDSLGCRLVFLLMQYCVAANYWLLVEGVY -250  
 HUM - LKWMYSTAAQQHQWDGLLSYQDSLSCRLVFLLMQYCVAANYWLLVEGVY - 81  
 RAT - LYTLFAFSVFSEQRIFKLYLSIGWGVPLLFVIPWGIVKYLYEDEGCWTRN -300  
 HUM - LYTLFAFSVFSEQWIFRLYVSIGWGVPLLFVVPWGIVKILYEDEGCWTRN -131  
 RAT - SNMNYWLIIRLPILFAIGVNFLVFIRVICIVIAKLANLMCKTDIKCRLA -350  
 HUM - SNMNYWLIIRLPILFAIGVNFLIFVRVICIVVSKLANLMCKTDIKCRLA -181  
 RAT - KSTLTLLIPLLGTHEVIFAFVMDEHARGTLRFVKLFTELSFTSFQGFMAV -400  
 HUM - KSTLTLLIPLLGTHEVIFAFVMDEHARGTLRFIKLFTELSFTSFQGLMAI -231  
 RAT - LYCFVNNEVQMEFRKSWERWRLERLNIQRDSSMKPLKCPTSSVSSGATVG -450  
 HUM - LYCFVNNEVQLEFRKSWERWRLHLHIQRDSSMKPLKCPTSSLSSGATAG -281  
 RAT - SSVYAATCQNSCS -463  
 HUM - SSMYTATCQASCS -294

FIG. 7



## INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP 93/00697

<b>I. CLASSIFICATION OF SUBJECT MATTER</b> (If several classification symbols apply, indicate all) <sup>6</sup>		
According to International Patent Classification (IPC) or to both National Classification and IPC		
Int.Cl. 5 C12N15/12;	C07K13/00;	C12N5/10; G01N33/74
<b>II. FIELDS SEARCHED</b>		
Minimum Documentation Searched <sup>7</sup>		
Classification System	Classification Symbols	
Int.Cl. 5	C12N ; C07K ; G01N	
Documentation Searched other than Minimum Documentation to the extent that such Documents are Included in the Fields Searched <sup>8</sup>		
<b>III. DOCUMENTS CONSIDERED TO BE RELEVANT<sup>9</sup></b>		
Category <sup>10</sup>	Citation of Document, <sup>11</sup> with indication, where appropriate, of the relevant passages <sup>12</sup>	Relevant to Claim No. <sup>13</sup>
P,X	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA. vol. 89, no. 18, 15 September 1992, WASHINGTON US pages 8641 - 8645 THORENS B; 'Expression cloning of the pancreatic beta cell receptor for the gluco-incretin hormone glucagon-like peptide 1.' see the whole document ---	1-18
A	FEBS LETTERS. vol. 267, no. 1, July 1990, AMSTERDAM NL pages 78 - 80 Richter G;Goke R;Goke B;Arnold R; 'Characterization of receptors for glucagon-like peptide-1(7-36)amide on rat lung membranes.' ---	1-18
<div style="display: flex; justify-content: space-between;"> <div> <p><sup>10</sup> Special categories of cited documents : <sup>10</sup></p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier document but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> </div> <div> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.</p> <p>"&amp;" document member of the same patent family</p> </div> </div>		
<b>IV. CERTIFICATION</b>		
Date of the Actual Completion of the International Search	Date of Mailing of this International Search Report	
12 JULY 1993	27.07.93	
International Searching Authority	Signature of Authorized Officer	
EUROPEAN PATENT OFFICE	NAUCHE S.A.	

III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)		
Category *	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claim No.
A	<p>FEBS LETTERS. vol. 262, no. 1, March 1990, AMSTERDAM NL pages 139 - 141 UTTENTHAL, L.O. ET AL; 'Characterization of high-affinity receptors for truncated glucagon-like peptide-1 in rat gastric glands.' see the whole document -----</p>	1-18